TCTAGACTGGACAGCATCCACAAGAGAAGCACCTAGAAGGAGAATTTTCCCCAGCAGCTTGCTCAGGACCC TGCAGGAGCCGCAGCTGGGACCTGCTGTTAACCATGAACTCTTCCTGCTGCCTGTCTTCTTTTCT $\tt CCGATGCTGCCTAACCTCTGAGCACCCTGCAGCCCTCCTGCCAGCAACCGGAGCGGCAGTGGGTTCTG$ TGATCCTGGCTGTGGTCAGGAATGGCAACCTGCACTCTCCCATGTACTTCTTCCTGTGCAGCCTGGCTGCA GCCGACATGCTGGTGAGCCTGTCCAACTCCCTGGAGACCATCATGATCGCCGTGATCAACAGCGACTCCCT GACCTTGGAGGACCAGTTTATCCAGCACATGGATAATATCTTCGACTCTATGATTTTGCATCTCCCTGGTGG $\tt CCTCCATCTGCAACCTCCTGGCCATTGCCATCGACAGGTACGTCACCATCTTCTATGCCCTTCGGTACCAC$ AGCATCATGACAGTTAGGAAAGCCCTCACCTTGATCGGGGTCATCTGGGTCTGCTGCGGCATCTGCGGCGT GATGTTCATCATCTCCGAGAGCAAGATGGTCATCGTGTGTCTCATCACCATGTTCTTCGCCATGGTGC TCCTCATGGGCACCCTATATATCCACATGTTCCTCTTCGCCAGGCTCCACGTCCAGCGCATCGCAGTGCTG $\tt CCCCCTGCTGGCGTGGTGGCCCCACAGCAGCACTCCTGCATGAAGGGGGCTGTCACCATCACTATCCTGCT$ GGGTGTTTTCATCTTCTGCTGGGCGCCTTTCTTCCTCCACCTGGTCCTCATCATCACCTGCCCCACCAATC $\tt CCCCTCATCTACGCCTTCCGCAGCCTGGAGCTGCGCAACACGTTCAAGGAGATTCTCTGCGGCTGCAACAG$ CATGAACTTGGGCTAGGATGCCCGTGGAGGTGTTCCACATCCAGCCAAGAGACAAAAACAACGCTCAGACG GGACGTAAAAGGGTGTTAGGAGCTGGAACTGTGCTTGGCTTCGTCTGTAAGCTCGTGGCCCTTTGCAGACG TGGAAGAATCAGGCAAAGCAGCCCTGAGTGTCATCTGTTCATTGCTAGGCACCCAGGGTTTGTGGCCCC TGCCTGCTTATTGGCTTTGTACCAGTAACTGTGCTTCAAGCCAACCAGACCGGAGGGCTCTCGTGAGCAGA AAGAGTGCTTAGACTTCCGGCAAGCATCCTGGCTCACAGCGGCCACCTCCTGACCACTACCGGGAGAGCTT TGCACATATTCTGTGGGAGATTGAGTGAAGCCCTGAAAACAATGTGATATTTGCTGCTCCCTTCCAGAACT TACATCTGTGCCAGCCTCCCGAACCCCTGCACAGAGACATGACCCCCTTCTCCCTGTGCCGTTGTCATGG TTGTTATTATTGTTGGAGTTTTGTTCGTTAAAATCTAAGCTT (SEQ ID NO:1)

MNSSCCLSSVSPMLPNLSEHPAAPPASNRSGSGFCEQVFIKPEVFLALGIVSLMENILVILAVVRNGNLHS PMYFFLCSLAAADMLVSLSNSLETIMIAVINSDSLTLEDQFIQHMDNIFDSMICISLVASICNLLAIAIDR YVTIFYALRYHSIMTVRKALTLIGVIWVCCGICGVMFIIYSESKMVIVCLITMFFAMVLLMGTLYIHMFLF ARLHVQRIAVLPPAGVVAPQQHSCMKGAVTITILLGVFIFCWAPFFLHLVLIITCPTNPYCICYTAHFNTY LVLIMCNSVIDPLIYAFRSLELRNTFKEILCGCNSMNLG (SEQ ID NO:2)

FIGURE 1

Underlined = deleted in targeting construct

Bold = sequence flanking Neo insert in targeting construct

TCTAGACTGGACAGCATCCACAAGAGAAGCACCTAGAAGGAGAATTTTCCCCAGCAGCTT GCTCAGGACCCTGCAGGAGCCGCAGCTGGGACTGGACCTGCTGTTAACCATGAACTCTTC CTGCTGCCTGTCTTCTGTTTCTCCGATGCTGCCTAACCTCTCTGAGCACCCTGCAGCCCC TCCTGCCAGCAACCGGAGCGGCAGTGGGTTCTGTGAGCAGGTCTTCATCAAGCCGGAGGT ${\tt CTTCCTGGCTCTGGCATCGTCAGTCTGATGGAAAACATCCTGGTGATCCTGGCTGTGGT}$ CAGGAATGGCAACCTGCACTCTCCCATGTACTTCTTCCTGTGCAGCCTGGCTGCAGCCGA CATGCTGGTGAGCCTGTCCAACTCCCTGGAGACCATCATGATCGCCGTGATCAACAGCGA CTCCCTGACCTTGGAGGACCAGTTTATCCAGCACATGGATAATATCTTCGACTCTATGAT TTGCATCTCCCTGGTGGCCTCCATCTGCAACCTCCTGGCCATTGCCATCGACAGGTACGT CACCATCTTCTATGCCCTTCGGTACCACAGCATCATGACAGTTAGGAAAGCCCTCACCTT GATCGGGGTCATCTGGGTCTGCTGCGGCATCTGCGGCGTGATGTTCATCATCTACTCCGA GAGCAAGATGGTCATCGTGTGTCTCATCACCATGTTCTTCGCCATGGTGCTCCTCATGGG CACCCTATATATCCACATGTTCCTCTTCGCCAGGCTCCACGTCCAGCGCATCGCAGTGCT GCCCCTGCTGGCGTGGCCCCACAGCAGCACTCCTGCATGAAGGGGGCTGTCACCAT CACTATCCTGCTGGGTGTTTTCATCTTCTGCTGGGCGCCTTTCTTCCTCCACCTGGTCCT CATCATCACCTGCCCCACCAATCCCTACTGCATCTGCTACACGGCCCATTTCAACACCTA CCTGGTTCTCATCATGTGCAACTCCGTCATCGACCCCCTCATCTACGCCTTCCGCAGCCT GGAGCTGCGCAACACGTTCAAGGAGATTCTCTGCGGCTGCAACAGCATGAACTTGGGCTA GGATGCCCGTGGAGGTGTTCCACATCCAGCCAAGAGACAAAAACAACGCTCAGACGGGAC ${\tt GTAAAAGGGTGTTAGGAGCTGGAACTGTGCTTGGCTTCGTCTGTAAGCTCGTGGCCCTTT}$ $\tt TTGATCTAGCACATAGCCTGGAAGAATCAGGCAAAGCAGCCCTGAGTGTCATCTGTGTTC$ ATTGCTAGGCACCCAGGGTTTGTGGCCCCTGCCTTATTGGCTTTGTACCAGTAACTG TGCTTCAAGCCAACCAGACCGGAGGGCTCTCGTGAGCAGAAAGAGTGCTTAGACTTCCGG CAAGCATCCTGGCTCACAGCGGCCACCTCCTGACCACTACCGGGAGAGCTTTGCACATAT TCTGTGGGAGATTGAGTGAAGCCCTGAAAACAATGTGATATTTGCTGCTCCCTTCCAGAA ${\tt CTTACATCTGTGCCAGCCTCCCCGAACCCCTGCACAGAGACATGACCCCCTTCTCCCTGT}$ GCCGTTGTCATGGTTGTTATTATTGTTGGAGTTTTTGTTCGTTAAAATCTAAGCTT

FIGURE 2A

Gene Sequence Structure *

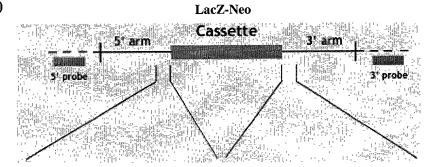
296 bp Sequence Deleted 519 bp

Size of CDS: 1675 bp

Targeting Vector* (genomic sequence)

Construct Number: 2787

Arm Length: 5': 1.6 kb **3**': 4 kb



5'>ACCTGCTGTTAACCATGAACT CTTCCTGCTGCCTGTCTTCTGTTT CTCCGATGCTGCCTAACCTCTCTG AGCACCCTGCAGCCCCTCCTGCCA GCAACCGGAGCGGCAGTGGGTTCT GTGAGCAGGTCTTCATCAAGCCGG AGGTCTTCCTGGCTCTGGGCATCG TCAGTCTGATGGAAAACATCCTGG TGATCCTGGCT<3' (SEO ID NO:3) 5'>CATTGCCATCGACAGGTACGT CACCATCTTCTATGCCCTTCGGTA CCACAGCATCATGACAGTGAGGAA AGCCCTCACCTTGATCGGGGTCAT CTGGGTCTGCTGCGGCATCTGCGG CGTGATGTTCATCATCTACTCCGA GAGCAAGATGGTCATCGTGTGTCT CATCACCATGTTCTTCGCCATGGT GCTCCTCATGG<3' (SEQ ID NO:4)

FIGURE 2B